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SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG
 <120> Method for the purification of an N-terminal fragment of
 hepatocyte growth factor
 <130> 22389 WO
 <150> EP 04004950.4
 <151> 2004-03-03
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 <170> PatentIn version 3.2
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 Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys
 20 25 30
 aaa gtg aat act gca gac caa tgt gct aat aga tgt act agg aat aaa 144
 Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys
 35 40 45
 gga ctt cca ttc act tgc aag gct ttt gtt ttt gat aaa gca aga aaa 192
 Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys
 50 55 60
 caa tgc ctc tgg ttc ccc ttc aat agc atg tca agt gga gtg aaa aaa 240
 Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys
 65 70 75 80
 gaa ttt ggc cat gaa ttt gac ctc tat gaa aac aaa gac tac att aga 288
 Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg
 85 90 95
 aac tgc atc att ggt aaa gga cgc agc tac aag gga aca gta tct atc 336
 Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile
 100 105 110

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Thr	Lys	Ser	Gly	Ile	Lys	Cys	Gln	Pro	Trp	Ser	Ser	Met	Ile	Pro	His	
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gaa	cac	agc	ttt	ttg	cct	tcg	agc	tat	cgg	ggc	aaa	gac	cta	cag	gaa	432
Glu	His	Ser	Phe	Leu	Pro	Ser	Ser	Tyr	Arg	Gly	Lys	Asp	Leu	Gln	Glu	
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aac	tac	tgt	cga	aat	cct	cga	ggg	gaa	gaa	ggg	gga	ccc	tgg	tgt	ttc	480
Asn	Tyr	Cys	Arg	Asn	Pro	Arg	Gly	Glu	Glu	Gly	Gly	Pro	Trp	Cys	Phe	
145					150					155					160	
aca	agc	aat	cca	gag	gta	cgc	tac	gaa	gtc	tgt	gac	att	cct	cag	tgt	528
Thr	Ser	Asn	Pro	Glu	Val	Arg	Tyr	Glu	Val	Cys	Asp	Ile	Pro	Gln	Cys	
				165					170					175		
tca	gaa	gtt	gaa	tgc	atg	acc	tgc	aat	ggg	gag	agt	tat	cga	ggc	ctc	576
Ser	Glu	Val	Glu	Cys	Met	Thr	Cys	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Leu	
			180					185					190			
atg	gat	cat	aca	gaa	tca	ggc	aag	att	tgt	cag	cgc	tgg	gat	cat	cag	624
Met	Asp	His	Thr	Glu	Ser	Gly	Lys	Ile	Cys	Gln	Arg	Trp	Asp	His	Gln	
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Thr	Pro	His	Arg	His	Lys	Phe	Leu	Pro	Glu	Arg	Tyr	Pro	Asp	Lys	Gly	
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Phe	Asp	Asp	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Gln	Pro	Arg	Pro	Trp	
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Cys	Tyr	Thr	Leu	Asp	Pro	His	Thr	Arg	Trp	Glu	Tyr	Cys	Ala	Ile	Lys	
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Thr	Ile	Trp	Asn	Gly	Ile	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Tyr	Pro	
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His	Glu	His	Asp	Met	Thr	Pro	Glu	Asn	Phe	Lys	Cys	Lys	Asp	Leu	Arg	
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tgt gat atg tca cat gga caa gat tgt tat cgt ggg aat ggc aaa aat      1104
Cys Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn
      355      360      365

tat atg ggc aac tta tcc caa aca aga tct gga cta aca tgt tca atg      1152
Tyr Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met
      370      375      380

tgg gac aag aac atg gaa gac tta cat cgt cat atc ttc tgg gaa cca      1200
Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro
      385      390      395      400

gat gca agt aag ctg aat gag aat tac tgc cga aat cca gat gat gat      1248
Asp Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp
      405      410      415

gct cat gga ccc tgg tgc tac acg gga aat cca ctc att cct tgg gat      1296
Ala His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp
      420      425      430

tat tgc cct att tct cgt tgt gaa ggt gat acc aca cct aca atc gtt      1344
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Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys
      35      40      45
Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys
      50      55      60

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Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys
65 70 75 80

Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg
85 90 95

Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile
100 105 110

Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His
115 120 125

Glu His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu
130 135 140

Asn Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe
145 150 155 160

Thr Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys
165 170 175

Ser Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu
180 185 190

Met Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln
195 200 205

Thr Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly
210 215 220

Phe Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp
225 230 235 240

Cys Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys
245 250 255

Thr Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr
260 265 270

Thr Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn
275 280 285

Thr Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro
290 295 300

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His Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg
305 310 315 320

Glu Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe
325 330 335

Thr Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn
340 345 350

Cys Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn
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Tyr Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met
370 375 380

Trp Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro
385 390 395 400

Asp Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp
405 410 415

Ala His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp
420 425 430

Tyr Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
435 440 445